

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	No.	Score	Match	Length	DB ID	
1	1693	99.7	365	2	A43720		parathion hydrolas
2	913	53.8	325	2	A28214		phosphotriesterase
3	448	26.4	326	2	D70962		hypothetical prote
4	408	24.0	314	2	F90424		hypothetical prote
5	385	22.7	323	2	E75459		probable phosphotr
6	331	19.5	305	2	AB1321		probable phosphotr
7	309	18.2	331	2	A83678		hypothetical prote
8	308	18.1	292	2	F65132		hypothetical 32.9
9	296	17.4	679	2	F83723		hypothetical prote
10	277.5	16.3	355	2	AD2933		hypothetical prote
11	277.5	16.3	355	2	C98349		resiniferatoxin-bi
12	273	16.1	344	2	AC0994		puative phophotrie
13	269.5	15.9	330	2	AG1405		Phosphotriesterase
14	268.5	15.8	330	2	AG1781		Phosphotriesterase
15	229	13.5	351	2	A99586		conserved hypothet

RESULT 1

A43720

parathion hydrolase precursor - *Flavobacterium* sp. (ATCC 27551)

C;Species: *Flavobacterium* sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 08-Oct-1999

C;Accession: A43720

R;Mulbry, W.W.; Kams, J.S.

J. Bacteriol. 171, 6740-6746, 1989

A;Title: Parathion hydrolase specified by the *Flavobacterium* opd gene: relationship between the gene and protein.

A;Reference number: A43720; MUID:90078122; PMID:2556372

A;Accession: A43720

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-365 <MUL>

A;Cross-references: GB:M29593; NID:g148712; PIDN:AAA24930.1; PID:g148713

A;Experimental source: ATCC 27551

Query Match 99.7%; Score 1693; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-126;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2

SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR
61

|||||

Db 30

SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR
89

Qy 62

ARAAGVRTIVDVSTFDIGRDVSLAEVSRAADVHIVAATGLWFDPLSMRLRSVEELTQF
121

|||||

Db 90

ARAAGVRTIVDVSTFDIGRDVSLAEVSRAADVHIVAATGLWFDPLSMRLRSVEELTQF
149

Qy 122

FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG
181

|||||

Db 150

FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG
209

Qy 182

EQQAIFESEGLSPSRVCIGHSDDTDDLSTALAAARGYLIGLDHIPHSAIGLEDNASAS
241

|||||

Db 210

EQQAIFESEGLSPSRVCIGHSDDTDDLSTALAAARGYLIGLDHIPHSAIGLEDNASAS
269

Qy 242

ALLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFIP
301

|||||

Db 270

ALLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFIP
329

Qy 302 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 337

|||||

Db 330 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 365

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1695	99.8	337	5	ABB79958	Abb79958 Organopho
2	1693	99.7	336	6	ABG72651	Abg72651 Flavobact
3	1693	99.7	365	2	AAR05573	Aar05573 Parathion
4	1693	99.7	365	6	ABB82802	Abb82802 Flavobact
5	1689	99.5	336	6	ABG72650	Abg72650 Flavobact
6	1686	99.3	357	2	AAY43487	Aay43487 Amino aci
7	1685	99.2	334	2	AAY43486	Aay43486 Amino aci
8	1558	91.8	356	6	ABB82799	Abb82799 A. radiob
9	1558	91.8	384	6	ABB82798	Abb82798 A. radiob
10	1552	91.4	384	6	ABB82801	Abb82801 A. radiob
11	1535	90.4	384	6	ABB82800	Abb82800 A. radiob
12	465	27.4	326	6	ABU33918	Abu33918 Protein e
13	448	26.4	326	6	ABU36432	Abu36432 Protein e
14	400	23.6	306	6	ABU34486	Abu34486 Protein e
15	372.5	21.9	346	6	ABU31613	Abu31613 Protein e
16	331	19.5	305	5	ABB48499	Abb48499 Listeria
17	331	19.5	305	6	ABU32460	Abu32460 Protein e
18	308	18.1	292	6	ABU14978	Abu14978 Protein e
19	283	16.7	345	6	ABU21704	Abu21704 Protein e
20	273	16.1	344	6	ABU47684	Abu47684 Protein e
21	273	16.1	344	6	ABU47288	Abu47288 Protein e
22	269.5	15.9	330	5	ABB47719	

RESULT 1

ABB79958

ID ABB79958 standard; protein; 337 AA.

XX

AC ABB79958;

XX

DT 12-DEC-2002 (first entry)

XX

DE Organophosphorous hydrolase.

XX

KW Organophosphorous hydrolase; OPH; enzyme; immobilisation;

KW chemical warfare; pesticide; pollutant; detoxification; decontamination.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Peptide 1. .29

FT /label= Signal_peptide

FT Protein 30. .337

FT /label= Mature_protein

XX

PN WO200268454-A2.

XX

PD 06-SEP-2002.

XX

PF 21-FEB-2002; 2002WO-US005755.

XX

PR 21-FEB-2001; 2001US-00791138.

PR 20-FEB-2002; 2002US-00081737.

XX

PA (BATT) BATTELLE MEMORIAL INST.

XX

PI Ackerman EJ, Liu J, Chenghong L;

XX

DR WPI; 2002-713364/77.

DR N-PSDB; ABQ81428.

XX

PT Protein system, for facilitating chemical reactions e.g. hydrolysis,

PT oxidation, hydrogenation and proteolysis, comprises porous matrix

PT material and protein within matrix.

XX

PS Example; Fig 4; 56pp; English.

XX

CC The present sequence is the protein sequence of an organophosphorous
 CC hydrolase (OPH) encoded by an expression plasmid of the invention. The
 CC invention provides a method for producing OPH by transfecting a host cell
 CC with a vector comprising a sequence encoding OPH linked to a T7
 CC expression control sequence, culturing the transfected host cell, and
 CC purifying OPH from the cell or culture medium. This OPH has an activity
 CC of about 13,000 U/mg. The host cell can be prokaryotic, e.g. Escherichia
 CC coli, or eukaryotic, e.g. Pichia pastoris. The invention also provides a
 CC protein system for facilitating chemical reactions. The protein system
 CC comprises a porous matrix material having a pore volume of which at least
 CC 90% is composed of pores of 50-400 Angstroms. The protein occupies 5-40%
 CC of the average pore volume, and is preferably an enzyme, especially OPH
 CC having an activity of 60-95% that of the active state and retaining about
 CC 10% of its activity after 24 hr under alkaline conditions. The porous

CC matrix may comprise surface hydroxyls that are reacted with a coupling
CC agent to form a functionalised monolayer. The system provides high enzyme
CC activities on a porous support, stability under a variety of conditions,
CC high densities of active protein and capability in industrial-scale
CC applications. It provides environmentally safe methods of destroying
CC chemical weapons and organophosphorous pesticides while avoiding the
CC dangers inherent in burning these materials. It can be used in filtration
CC equipment for individual soldiers and pesticide workers, and in vehicles,
CC aircraft, ships and buildings such as civilian and military defence
CC shelters, to perform detoxifications

XX

SQ Sequence 337 AA;

Query Match 99.8%; Score 1695; DB 5; Length 337;
Best Local Similarity 99.7%; Pred. No. 1.1e-163;
Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MSIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLR 60
          |||
Db      1 MSIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLR 60

Qy     61 RARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHIVAATGLWFDPPLSMRLRSVEELTQ 120
          |||
Db     61 RARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHIVAATGLWFDPPLSMRLRSVEELTQ 120

Qy    121 FFLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRD 180
          |||
Db    121 FFLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRD 180

Qy    181 GEQQAAIFESEGLSPSRVCIGHSDDTDDLSTALAAARGYLIGLDHIPHSAIGLEDNASA 240
          |||
Db    181 GEQQAAIFESEGLSPSRVCIGHSDDTDDLSTALAAARGYLIGLDHIPHSAIGLEDNASA 240

Qy    241 SALLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFI 300
          |||
Db    241 SALLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFI 300

Qy    301 PLRVIPFLREKGVPOETLAGITVTNPARFLSPTLRAS 337
          |||
Db    301 PLRVIPFLREKGVPOETLAGITVTNPARFLSPTLRAS 337
```

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1688	99.4	365	2	Q8GC45	Q8gc45 flavobacter	
2	1630	96.0	365	2	Q8VLR0	Q8vlr0 chryseobact	
3	1558	91.8	384	2	Q93LD7	Q93ld7 agrobacteri	
4	915	53.9	325	2	Q47934	Q47934 flavobacter	
5	448	26.4	326	16	Q7U2I4	Q7u2i4 mycobacteri	
6	408	24.0	314	17	Q97VT7	Q97vt7 sulfolobus	
7	385	22.7	323	16	Q9RVU2	Q9rvu2 deinococcus	
8	331	19.5	305	16	Q8Y5T5	Q8y5t5 listeria mo	
9	325.5	19.2	362	16	Q985I1	Q985i1 rhizobium l	
10	309	18.2	331	16	Q9KG87	Q9kg87 bacillus ha	
11	306	18.0	292	16	Q8FCW5	Q8fcw5 escherichia	
12	304	17.9	292	16	Q7UAS1	Q7uas1 shigella fl	
13	296	17.4	679	16	Q9KF95	Q9kf95 bacillus ha	
14	288	17.0	344	16	Q8FG90	Q8fg90 escherichia	
15	277.5	16.3	355	16	Q8UBF0	Q8ubf0 agrobacteri	
16	273	16.1	344	16	Q8XFU6	Q8xfu6 salmonella	
17	270.5	15.9	349	13	Q7SZS2	Q7szs2 xenopus lae	
18	269.5	15.9	330	16	Q8Y427	Q8y427 listeria mo	
19	268.5	15.8	330	16	Q927J1	Q927j1 listeria in	

RESULT 1

Q8GC45

ID Q8GC45 PRELIMINARY; PRT; 365 AA.
 AC Q8GC45;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Parathion hydrolase precursor (EC 3.1.8.1).
 GN OPD.
 OS Flavobacterium sp. ATCC 27551.
 OG Plasmid pPDL2.
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
 OC Flavobacteriaceae; Flavobacterium.
 OX NCBI_TaxID=74567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27551;
 RA Siddavatham D., Manavathi B., Merrick M.;
 RT "The conserved region surrounding the organophosphorus pesticide
 RT degrading (opd) gene on the Flavobacterium plasmid pPDL2 has the
 RT features of a complex transposon.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ421424; CAD13181.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0004063; F:aryldialkylphosphatase activity; IEA.
 DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009056; P:catabolism; IEA.
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR InterPro; IPR001559; PTE.
 DR Pfam; PF02126; PTE; 1.
 DR PROSITE; PS01322; PHOSPHOTRIESTERASE_1; 1.
 DR PROSITE; PS01323; PHOSPHOTRIESTERASE_2; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Signal; Hydrolase; Plasmid.
 FT SIGNAL 1 29
 SQ SEQUENCE 365 AA; 38973 MW; 0C92FE577BFE4FB0 CRC64;

Query Match 99.4%; Score 1688; DB 2; Length 365;
 Best Local Similarity 99.7%; Pred. No. 8.6e-124;
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 61
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 Db 30 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 89
 Qy 62 ARAAGVRTIVDVSTFDIGRDVSLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF 121
 |||
 Db 90 ARAAGVRTIVDVSTFDIGRDVSLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF 149
 Qy 122 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 181
 |||
 Db 150 FLREIQYGIEDTGIRAGIIKVATTGKAAPFQELVLKAAARASLATGVPVTTHTAASQRDG 209
 Qy 182 EQQAAIFESEGLSPSRVCIGHSDDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS 241
 |||
 Db 210 EQQAAIFESEGLSPSRVCIGHSDDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS 269

Qy	242	ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP	301
Db	270	ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP	329
Qy	302	LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS	337
Db	330	LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS	365

O8VLR0

Query Match 96.0%; Score 1630; DB 2; Length 365;
Best Local Similarity 96.4%; Pred. No. 3e-119;
Matches 324; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy	2	SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	61
		:	
Db	30	SIGTGDRINTVRGPITNSEAGFTLTHEHICGTSAGFLRAWQEFGSRKALAEKAVRGLRR	89
Qy	62	ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHI VAATGLWFDPPLSMRLRSVEELTQF	121
		: : :	
Db	90	ARAAGVRTIVDVSTFDIGRDVSLLAEVSMMVDVSLLAETGLWFDPPLSIGLRSVEELTQF	149
Qy	122	FLREIQYGI EDTGIRAGI I KVATTGKATPFQELVLKAAARASLATGVPTTTHTAASQRDG	181
Db	150	FLREIQYGI EDTGIRAGI I KVATTGKATPFQELVLKAAARASLATGVPTTTHTAASQRDG	209
Qy	182	EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS	241
Db	210	EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS	269
Qy	242	ALLGIRSWQTRALLIKALIDOGYMKOILVSNDFLGFSSSYVTNIMDVMDRVNPDGMAFI P	301

Db 270 |||||ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFSGFSSYVTNIMDVMDRVNPDGMAFIP 329

Qy 302 LRVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 337

Db 330 |||||LRVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 365

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1689	99.5	336	4	US-09-603-450-4	Sequence 4, Appli
2	1688	99.4	365	6	5484728-2	Patent No. 5484728
3	267	15.7	352	4	US-09-543-681A-8100	Sequence 8100, Ap
4	238.5	14.0	349	1	US-08-343-027A-12	Sequence 12, Appl
5	105	6.2	477	4	US-09-489-039A-9937	Sequence 9937, Ap
6	104	6.1	495	4	US-09-252-991A-21509	Sequence 21509, A
7	99.5	5.9	2482	4	US-09-252-991A-16967	Sequence 16967, A
8	92	5.4	908	4	US-09-328-352-7168	Sequence 7168, Ap
9	91.5	5.4	461	4	US-09-134-000C-5551	Sequence 5551, Ap
10	90.5	5.3	647	4	US-09-725-735A-18	Sequence 18, Appl
11	90	5.3	569	4	US-09-543-681A-5106	Sequence 5106, Ap
12	89.5	5.3	1161	4	US-09-252-991A-22872	Sequence 22872, A
13	89	5.2	403	4	US-09-252-991A-25706	Sequence 25706, A
14	89	5.2	655	4	US-09-107-532A-4425	Sequence 4425, Ap
15	88.5	5.2	283	4	US-09-543-681A-8240	Sequence 8240, Ap
16	87	5.1	288	4	US-09-252-991A-18721	Sequence 18721, A
17	87	5.1	476	4	US-09-489-039A-14013	Sequence 14013, A

RESULT 1

US-09-603-450-4

; Sequence 4, Application US/09603450

; Patent No. 6469145

; GENERAL INFORMATION:

; APPLICANT: Rastogi, Vipin K

; APPLICANT: Cheng, Tu-c

; APPLICANT: DeFrank, Joseph J

; TITLE OF INVENTION: One-Step Purification Process for Organophosphorus

; TITLE OF INVENTION: Hydrolase Enzyme

; FILE REFERENCE: DAM-508-99

; CURRENT APPLICATION NUMBER: US/09/603,450

; CURRENT FILING DATE: 2000-06-26

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 336

; TYPE: PRT

; ORGANISM: Flavobacterium sp

US-09-603-450-4

Query Match 99.5%; Score 1689; DB 4; Length 336;

Best Local Similarity 100.0%; Pred. No. 4.7e-174;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3	IGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRA	62
Db	2	IGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRA	61
Qy	63	RAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHI VAATGLWFDPP	122
Db	62	RAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHI VAATGLWFDPP	121
Qy	123	LREIQYGI EDTGIRAGIIKV	ATTGKATPFQELVLKAAARAS	182
Db	122	LREIQYGI EDTGIRAGIIKV	ATTGKATPFQELVLKAAARAS	181
Qy	183	QQAAIFESEGLSPSRVCIGH	SDDTDDLSYLTALAARGYLIG	242
Db	182	QQAAIFESEGLSPSRVCIGH	SDDTDDLSYLTALAARGYLIG	241
Qy	243	LLGIRSWQTRALLIKALIDQ	GYMKQILVSNWDLFGFSSY	302
Db	242	LLGIRSWQTRALLIKALIDQ	GYMKQILVSNWDLFGFSSY	301
Qy	303	RVIPFLREKGV PQETLAGIT	VTNPARFLSPTLRAS	337
Db	302	RVIPFLREKGV PQETLAGIT	VTNPARFLSPTLRAS	336

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1693	99.7	365	1	OPD_FLASP	P16648	flavobacter
2	448	26.4	326	1	PHP_MYCTU	P96413	mycobacteri
3	308	18.1	292	1	PHP_ECOLI	P45548	escherichia
4	243.5	14.3	349	1	PTER_HUMAN	Q96bw5	homo sapien
5	242.5	14.3	349	1	PTER_RAT	Q63530	rattus norv
6	239.5	14.1	349	1	PTER_MOUSE	Q60866	mus musculu
7	211.5	12.5	350	1	PTER_DROME	Q9vhf2	drosophila
8	127	7.5	216	1	YE97_MYCPN	P75290	mycoplasma
9	103	6.1	226	1	GPH2_PSEAE	Q9hz62	pseudomonas
10	103	6.1	319	1	HE31_STRCO	Q9wx16	streptomyce
11	96	5.7	342	1	ARGC_STRCO	P54895	streptomyce
12	93.5	5.5	352	1	TFTE_BURCE	Q45072	burkholderi
13	93	5.5	3421	1	TEGU_HSVEB	P28955	equine herp
14	92.5	5.4	522	1	LEU1_DEIRA	Q9rua9	deinococcus
15	92.5	5.4	898	1	SYA_METTH	Q27718	methanobact
16	92	5.4	486	1	LE11_PYRAB	Q9uz08	pyrococcus
17	92	5.4	617	1	VATA_MANSE	P31400	manduca sex
18	91.5	5.4	494	1	TYRO_RHIME	P33180	rhizobium m
19	91.5	5.4	520	1	LEU1_YERPE	Q8zig8	yersinia pe
20	91.5	5.4	1139	1	VRNA_BSMV	P17595	barley stri
21	91	5.4	1290	1	RPOC_MYCPN	P75271	mycoplasma
22	90.5	5.3	333	1	YF72_HALN1	Q9hpl8	halobacteri
23	90.5	5.3	838	1	GLGB_STRAW	Q82jf0	streptomyce
24	89.5	5.3	300	1	Y505_MYCLE	Q49823	mycobacteri
25	89.5	5.3	308	1	Y505_MYCTU	Q11169	mycobacteri
26	89.5	5.3	435	1	PROA_BRAJA	Q89x85	bradyrhizob
27	89.5	5.3	958	1	GCP2_PSEAE	Q9htx7	pseudomonas
28	89	5.2	614	1	VAA2_DROME	Q27331	drosophila

RESULT 1

OPD_FLASP

ID OPD_FLASP STANDARD; PRT; 365 AA.
AC P16648; P13739;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Parathion hydrolase precursor (EC 3.1.8.1) (Phosphotriesterase)
DE (PTE).
GN OPD.
OS Flavobacterium sp. (strain ATCC 27551), and
OS Brevundimonas diminuta (Pseudomonas diminuta).
OG Plasmid pCMS1.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Flavobacterium.
OX NCBI_TaxID=239, 293;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-53.
RC SPECIES=Flavobacterium sp ATCC 27551;
RX MEDLINE=90078122; PubMed=2556372;
RA Mulbry W.W., Cairns J.S.;
RT "Parathion hydrolase specified by the Flavobacterium opd gene:
RT relationship between the gene and protein.";
RL J. Bacteriol. 171:6740-6746(1989).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-44.
RC SPECIES=B.diminuta; STRAIN=MG;
RA Serdar C.M., Murdock D.C., Rohde M.F.;
RT "Parathion hydrolase gene from Pseudomonas diminuta MG: subcloning,
RT complete nucleotide sequence, and expression of the mature portion of
RT the enzyme in Escherichia coli.";
RL Biotechnology 7:1151-1155(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.diminuta; STRAIN=MG;
RX MEDLINE=88198028; PubMed=2834339;
RA McDaniel C.S., Harper L.L., Wild J.R.;
RT "Cloning and sequencing of a plasmid-borne gene (opd) encoding a
RT phosphotriesterase.";
RL J. Bacteriol. 170:2306-2311(1988).
RN [4]
RP ACTIVE SITE.
RX MEDLINE=94206935; PubMed=8155644;
RA Kuo J.M., Raushel F.M.;
RT "Identification of the histidine ligands to the binuclear metal
RT center of phosphotriesterase by site-directed mutagenesis.";
RL Biochemistry 33:4265-4272(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES=B.diminuta;
RX MEDLINE=95092756; PubMed=7999757;
RA Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;
RT "Three-dimensional structure of phosphotriesterase: an enzyme capable
RT of detoxifying organophosphate nerve agents.";
RL Biochemistry 33:15001-15007(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC SPECIES=B.diminuta;
 RX MEDLINE=95315185; PubMed=7794910;
 RA Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;
 RT "Three-dimensional structure of the binuclear metal center of
 RT phosphotriesterase.";
 RL Biochemistry 34:7973-7978(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC SPECIES=B.diminuta;
 RX MEDLINE=96214508; PubMed=8634243;
 RA Vanhooke J.L., Benning M.M., Raushel F.M., Holden H.M.;
 RT "Three-dimensional structure of the zinc-containing
 RT phosphotriesterase with the bound substrate analog diethyl
 RT 4-methylbenzylphosphonate.";
 RL Biochemistry 35:6020-6025(1996).
 CC -!- FUNCTION: Has an unusual substrate specificity for synthetic
 CC organophosphate triesters and phosphorofluoridates. All of the
 CC phosphate triesters found to be substrates are synthetic
 CC compounds. The identity of any naturally occurring substrate for
 CC the enzyme is unknown. Has no detectable activity with phosphate
 CC monoesters or diesters and no activity as an esterase or protease.
 CC It catalyzes the hydrolysis of the insecticide paraoxon at a rate
 CC approaching the diffusion limit and thus appears to be optimally
 CC evolved for utilizing this synthetic substrate.
 CC -!- CATALYTIC ACTIVITY: Aryl dialkyl phosphate + H(2)O = dialkyl
 CC phosphate + an aryl alcohol.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit.
 CC -!- PATHWAY: Pesticide detoxification.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- BIOTECHNOLOGY: Has attracted interest because of its potential use
 CC in the detoxification of chemical waste and warfare agents and its
 CC ability to degrade agricultural pesticides such as parathion.
 CC -!- SIMILARITY: Belongs to the phosphotriesterase family.
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to multiple
 CC sequencing errors.
 CC -----
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 DR EMBL; M29593; AAA24930.1; -.
 DR EMBL; M20392; AAA98299.1; ALT_FRAME.
 DR PIR; A28214; A28214.
 DR PIR; A43720; A43720.
 DR PDB; 1DPM; 20-AUG-97.
 DR PDB; 1EYW; 20-DEC-00.
 DR PDB; 1EZ2; 20-DEC-00.
 DR PDB; 1HZY; 04-APR-01.
 DR PDB; 1IOB; 04-APR-01.
 DR PDB; 1IOD; 04-APR-01.
 DR PDB; 1JGM; 04-JUL-01.
 DR PDB; 1PSC; 01-APR-97.

DR PDB; 1PTA; 01-DEC-95.
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR InterPro; IPR001559; PTE.
 DR Pfam; PF02126; PTE; 1.
 DR PROSITE; PS01322; PHOSPHOTRIESTERASE_1; 1.
 DR PROSITE; PS01323; PHOSPHOTRIESTERASE_2; 1.
 KW Hydrolase; Membrane; Plasmid; Signal; Metal-binding; Zinc;
 KW 3D-structure.

FT	SIGNAL	1	29	
FT	CHAIN	30	365	PARATHION HYDROLASE.
FT	METAL	55	55	ZINC 1.
FT	METAL	57	57	ZINC 1.
FT	METAL	169	169	ZINC 1 AND 2.
FT	METAL	201	201	ZINC 2.
FT	METAL	230	230	ZINC 2.
FT	METAL	301	301	ZINC 1.
FT	STRAND	36	39	
FT	TURN	40	41	
FT	STRAND	42	45	
FT	HELIX	46	49	
FT	STRAND	51	56	
FT	STRAND	59	60	
FT	TURN	63	64	
FT	HELIX	65	68	
FT	HELIX	70	73	
FT	HELIX	76	92	
FT	TURN	93	94	
FT	STRAND	95	100	
FT	HELIX	104	106	
FT	TURN	107	107	
FT	HELIX	110	120	
FT	TURN	121	121	
FT	STRAND	123	125	
FT	STRAND	127	129	
FT	HELIX	136	139	
FT	TURN	140	140	
FT	HELIX	143	155	
FT	TURN	156	156	
FT	STRAND	158	158	
FT	TURN	159	162	
FT	STRAND	163	163	
FT	STRAND	167	171	
FT	HELIX	178	194	
FT	STRAND	198	201	
FT	HELIX	204	206	
FT	TURN	207	207	
FT	HELIX	208	218	
FT	TURN	219	220	
FT	HELIX	223	225	
FT	STRAND	226	228	
FT	HELIX	231	233	
FT	HELIX	237	246	
FT	TURN	247	247	
FT	STRAND	249	252	
FT	TURN	255	256	
FT	TURN	260	261	
FT	TURN	263	264	

FT	HELIX	266	272
FT	HELIX	277	289
FT	TURN	290	291
FT	HELIX	293	295
FT	STRAND	296	298
FT	STRAND	305	306
FT	TURN	311	312
FT	HELIX	313	320
FT	TURN	322	323
FT	HELIX	324	326
FT	HELIX	327	330
FT	TURN	331	331
FT	HELIX	332	338
FT	TURN	339	340
FT	HELIX	343	350
FT	TURN	351	351
FT	HELIX	352	358
SQ	SEQUENCE	365 AA;	39003 MW; 41FF8E4B029B46DC CRC64;

Query Match 99.7%; Score 1693; DB 1; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4.1e-128;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	61
Db	30	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	89
Qy	62	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHI VAATGLWFDPPLSMRLRSVEELTQF	121
Db	90	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHI VAATGLWFDPPLSMRLRSVEELTQF	149
Qy	122	FLREIQYGI EDTGIRAGIIKVAT	TGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG	181
Db	150	FLREIQYGI EDTGIRAGIIKVAT	TGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG	209
Qy	182	EQQAIFESEGLSPSRVCIGHSD	DDTDDL SYLTALAARGYLIGLDHI PHSAIGLEDNASAS	241
Db	210	EQQAIFESEGLSPSRVCIGHSD	DDTDDL SYLTALAARGYLIGLDHI PHSAIGLEDNASAS	269
Qy	242	ALLGIRSWQTRALLIKALIDQGY	MKQILVSN DWLFGFSSYVTNIMDVMDRVNPDGMAFIP	301
Db	270	ALLGIRSWQTRALLIKALIDQGY	MKQILVSN DWLFGFSSYVTNIMDVMDRVNPDGMAFIP	329
Qy	302	LRVIPFLREKGV PQETLAGITV	TNPARFLSPTLRAS	337
Db	330	LRVIPFLREKGV PQETLAGITV	TNPARFLSPTLRAS	365